Index to Volume 81

ABO, 23–42
"Accuracy of Molecular Dating with the Rho Statistic: Deviations from Coalescent Expectations Under a Range of Demographic Models" (reprint), 911–933
advection, 121–140
African Americans, 71–88
agent-based models, 181–210, 237–258, 381–384
age patterns of mortality, 575–578
agricultural spread, 339–355
Aldenhovener Platte, 339–355, 357–380
Aleutian Islands, 407–426
Alfaro, E. L., 447–461
Allee effect, 121–140
allometry, 579–594
Almasy, L., 829–847, 853–867
Alpine populations, 875–898
Alu, 875–898
Amazonia, 71–88
amelogenin, 427–445
"American Indian Prehistory as Written in the Mitochondrial DNA: A Review" (reprint), 509–521
Amerindians, 59–69. *See also specific populations*
AmpFlSTR Identifiler, 427–445
analytical models, 237–258
anatomically modern humans, 211–235
ancient DNA, 407–426
anomalous and stratified diffusion, 121–140
Arbesú, I., 869–874
archaeological demography, 275–286
"Archaeological Demography," 275–286
Argentina, 59–69, 447–461
ascertainment, 663–728
assortative mating, 89–95
Austerlitz, F., 657–662
Automated Similarity Judgment Program (ASJP), 259–274
"Autosomal STR Analyses in Native Amazonian Tribes Suggest a Population Structure Driven by Isolation by Distance," 71–88
autosomal STRs, 71–88
Awa-Guajá, 71–88
Bailliet, G., 447–461
Bandkeramik settlements, 357–380
Baravelli, V., 625–638
Barbujani, G., 1–2, 625–638
Barrai, I., 447–461
Basques, 23–42
Bauduer, F., 23–42
Bayesian inference, 141–157
Bayesian quantitative trait nucleotide (BQTN) analysis, 829–847, 849–852, 869–874
behavioral genetics, 3–11
Belorussians, 43–58
Benin, 899–909
Bentley, R. A., 159–179
Bettinger, R. L., 211–235
binomial distribution, 13–22
biological distance, 579–594
biological invasions, 121–140
birth control, 3–11
birth weight, 463–477, 753–772, 773–776
"Birth-Weight-Specific Infant and Neonatal Mortality: Effects of Heterogeneity in the Birth Cohort" (reprint), 753–772
Blangero, J., 523–546, 547–550, 829–847, 849–852, 853–867
Bocquet-Appel, J. P., 287–307
Boyd, R., 211–235
Boyko, 43–58
Bromme culture, 309–337
Bronberg, R. A., 447–461
Buenos Aires, 447–461

Cabana, G. S., 407–426
Callegari-Jacques, S. M., 71–88
Canada, 645–655, 657–662
carbon-14 dating, 309–337
cardiovascular disease, 853–867
Carlton, M. A., 3–11
Carpathian Mountains, 43–58
carrying capacity, 105–119, 121–140, 211–235, 287–307
Cartault, F., 495–500
Castilla, E. E., 447–461
Cavalli-Sforza and Edwards distance, 389–406
CCR5 gene, 23–42

central Europe, 43–58
CFTR gene, 23–42
Chamberlain, A., 275–286
Chikhi, L., 625–638, 639–643
chimpanzees, 799–803
Chodick, G., 463–477
"Climate and Demography in Early Prehistory: Using Calibrated ^{14}C Dates as Population Proxies," 309–337
climate change, 287–307
climatic stress, 309–337
clinal patterns, 639–643
"Clinal Variation in the Nuclear DNA of Europeans" (reprint), 625–638
clotting factor VII, 853–867
coefficient of consanguinity, 447–461
colonization, 159–179
Colonna, V., 447–461
Coltrain, J. B., 407–426
common variant/common disease (CVCD) hypothesis, 729–733
"Comparison of Genetic Distance Measures Using Human SNP Genotype Data," 389–406
"Complete Mitochondrial Sequences for Haplogroups M23 and M46: Insights into the Asian Ancestry of the Malagasy Population" (brief communication), 495–500
complex disease, 663–728, 869–874
complex disease genetics, 729–733
complex segregation analysis, 523–546
Coppa, A., 479–493
Copper Age, 479–493
Córdoba (Argentina), 59–69
Cox, M. P., 911–933
Croatians, 43–58
CSF1PO, 71–88, 427–445
Cucina, A., 479–493
cultural evolution, 211–235, 597–619
cultural innovation, 211–235
"Cultural Innovations and Demographic Change," 211–235
cultural transmission, 105–119; of fertility, 657–662
Czechs, 43–58

D2S1338, 427–445
D3S1358, 71–88, 427–445
D5S818, 71–88, 427–445
D7S820, 71–88, 427–445
D8S1179, 71–88, 427–445
D13S317, 71–88, 427–445
D16S539, 71–88, 427–445
D18S51, 71–88, 427–445
D19S433, 427–445
D21S11, 71–88, 427–445
Degioanni, A., 23–42
De Grandi, A., 875–898
Demarchi, D. A., 59–69
demic diffusion, 159–179, 339–355
demographic history, 875–898
demography, 105–119, 309–337, 381–384
"Demography and Archaeology," 381–384
"Demography and Language Competition," 181–210
density-dependent dispersal, 121–140
dental affinity, 479–493
dental morphology, 479–493
Deoitch, Y., 463–477
Destro-Bisol, G., 625–638
DF508 mutation, 23–42
dietary components, 575–578
Dipierri, J. E., 447–461
dispersal, 105–119
Dobosz, M., 625–638
Dos Santos, S. E. B., 71–88
Dossou-Yovo, O. P., 899–909
drift, 23–42, 645–655
Dubey, B., 427–445
Dubut, V., 495–500
Ducrocq, R., 899–909
Duffy, 23–42
Dutour, O., 23–42
Dyer, T. D., 829–847

Eaaswarkhanth, M., 427–445
eastern Europe, 43–58
Editorial, 1–2
effective population size, 805–824
"Effects of Ascertainment Bias on Recovering Human Demographic History" (reprint), 735–751
Elion, J., 899–909
Eller, E., 735–751, 805–824
errata, 501
"Estimations of Population Density for Selected Periods Between the Neolithic and AD 1800," 357–380
ethnography, 159–179
Europe, 105–119, 339–355. *See also specific countries and populations*
evolutionary demography, 339–355
"Evolutionary Demography and the Population History of the European Early Neolithic," 339–355
evolutionary theory, 579–594
Excoffier, L., 141–157

experimental design, 663–728
extinction, 805–824

F7 gene, 853–867, 869–874
"The *F7* Gene and Clotting Factor VII Levels: Dissection of a Human Quantitative Trait Locus" (reprint), 853–867
factor V Leiden, 23–42
factor VII variability, 869–874
factor XI deficiency, 23–42
family planning, 3–11
family size, 3–11
family structure, 3–11
family studies, 547–550
fertility, 275–286
FGA, 427–445
finite mixtures of logistic regressions, 753–772
Fisher-KPP reaction-diffusion system, 121–140
Flash, S., 463–477
Fontcuberta, J., 853–867
founder effect, 23–42, 645–655
F_{ST}, 777–798, 799–803

Gage, T. B., 551–574, 575–578, 753–772, 773–776
GAIT Study, 853–867, 869–874
García, A., 59–69
Garenne, M., 97–100
Gavião, 71–88
gene flow, 23–42, 71–88
gene identity, 777–798
gene mapping, 729–733
"Gene Mapping in the 20th and 21st Centuries: Statistical Methods, Data Analysis, and Experimental Design" (reprint), 663–728
genetic affinities, 427–445
Genetic Analysis of Idiopathic Thrombophilia (GAIT) Project, 853–867, 869–874
genetic correlation, 595–596
genetic dating, 911–933
genetic distance, 389–406
genetic distance measures, 389–406
genetic diversity, 71–88, 141–157, 799–803
genetic drift, 657–662
genetic structure, 447–461
"Genetic Structure in Contemporary South Tyrolean Isolated Populations Revealed by Analysis of Y-Chromosome, mtDNA, and *Alu* Polymorphisms" (reprint), 875–898
genetic variation, 825–828
genotype-environment interaction, 523–546, 547–550
geographic difference in seasonality, 463–477
Germany, 357–380
gestational age, 773–776
Göring, H. H. H., 663–728, 729–733, 829–847

haplogroup, 59–69, 495–500; *see also* mitochondrial DNA haplogroups
haplogroup frequency, 43–58
Haque, I., 427–445
Hauchecorne, M., 899–909
Hawks, J., 805–824, 825–828
Hayes, M. G., 407–426
hemostasis, 853–867
Heyer, E., 1–2, 645–655, 657–662
HFE gene, 23–42
hierarchical models, 799–803
Hilpert, J., 357–380
historical linguistics, 381–384
HIV, 899–909
HLA, 23–42
Holden, C., 597–619
Holman, E. W., 259–274
Huff, C., 407–426
human adaptability, 547–550
human demographic history, 805–824
human dispersal, 159–179
"Human Dispersals: Mathematical Models and the Archaeological Record," 121–140
human evolution, 141–157
"Human Genetic Diversity and the Nonexistence of Biological Races" (reprint), 777–798
Human Genome Diversity Panel (HGDP), 389–406
human longevity, 275–286
human population dispersal, 121–140
Hungarians, 43–58
hunter-gatherers, 825–828
Hutsul, 43–58
Hutz, M. H., 71–88

ideal despotic distribution, 339–355
inbreeding, 825–828
"Incidence and Distribution of Native American mtDNA Haplogroups in Central Argentina," 59–69
India, 427–445
infant mortality, 753–772, 773–776
"Inferring Past Demography Using Spatially Explicit Population Genetic Models," 141–157
"Inferring Population Continuity Versus Replacement with aDNA: A Cautionary Tale from the Aleutian Islands," 407–426
inherited disorders, 645–655
intermarriage, 159–179

intermediate phenotypes, 869–874
"Introduction: Demography and Cultural Macroevolution," 105–119
introgression, 141–157
Ireland, 309–337
isonymy, 447–461
isonymy distances, 447–461
"Isonymy Structure of Buenos Aires City," 447–461
"Italian Populations During the Copper Age: Assessment of Biological Affinities Through Morphological Dental Traits," 479–493
Italy, 89–95, 479–493

James, W. H., 13–22
June, C. M., 43–58
juvenility index, 275–286

Kandler, A., 181–210
Kent, J. W., Jr., 829–847
kinship, 159–179
"Kinship, Marriage, and the Genetics of Past Human Dispersals," 159–179
Kittles, R. A., 777–798
Kochkin, I. T., 43–58
Konigsberg, L. W., 579–594, 595–596
Krishnamoorthy, R., 899–909

lactase persistence, 621–624
lactose digestion capacity, 597–619
lactose tolerance, 621–624
Ladins, 875–898
language, 621–624
language change, 105–119, 237–258
language competition, 181–210
language contact, 237–258
language evolution, 237–258, 259–274
language extinction, 181–210
language maintenance, 181–210
language origins, 237–258
language size, 259–274
Lapoumeroulie, C., 899–909
Lassek, W., 3–11
Latter's distance, 389–406
Layton, R. H., 159–179
LBK (Linear Pottery Culture), 339–355, 357–380
Lemko, 43–58
Levenshtein distance, 259–274
lexicostatistics, 259–274
Lexis (Lexian) variation, 13–22
Libiger, O., 389–406
likelihood analysis, 663–728
linkage, 663–728
linkage disequilibrium, 657–662, 663–728
linkage studies, 849–852
lithic industry, 287–307
"Local Extinction and Recolonization, Species Effective Population Size, and Modern Human Origins" (reprint), 805–824
Long, J. C., 777–798, 799–803
Lotka-Volterra system, 121–140

Mace, R., 597–619, 621–624
Madagascar, 495–500
Malagasy population, 495–500
Manfredini, M., 89–95
Manni, F., 1–2
mannose-binding lectin, 899–909
marital distance, 89–95
mate choice, 89–95
maternal age, 773–776
maternal lineages, 59–69
Mayr, A., 875–898
MBL2, 899–909
McBain, I., 43–58
"Mechanisms and Microevolutionary Consequences of Social Homogamy in a 19th-Century Italian Community" (brief communication), 89–95
"Medical Genetic Polymorphisms as Markers of Evolutionary Forces Within the Human Genome: Hypotheses Focusing on Natural Selection in the Basque Population," 23–42
medical genetics, 23–42
Meganathan, P. R., 427–445
Meitinger, T., 875–898
meningitis, 899–909
Mesolithic, 309–337
"Microsatellite Diversity Delineates Genetic Relationships of Shia and Sunni Muslim Populations of Uttar Pradesh, India," 427–445
migration history, 389–406
migration pattern, 159–179
mitochondrial DNA (mtDNA), 495–500, 875–898, 911–933
mitochondrial DNA distribution, 159–179
mitochondrial DNA haplogroups, 23–42, 59–69, 407–426; *see also* haplogroup
mitochondrial DNA polymorphism, 43–58
"Mitochondrial DNA Sequence Variation in the Boyko, Hutsul, and Lemko Populations of the Carpathian Highlands," 43–58
model averaging, 829–847
"Modeling Interactions Between Language Evolution and Demography," 237–258

modern human origins, 805–824
molecular chronology, 911–933
molecular genetics, 381–384
mortality, 275–286, 575–578
"The Most Widely Publicized Gender Problem in Human Genetics," 3–11
mtDNA. *See* mitochondrial DNA
Mueller, J. C., 875–898
"Multivariate Quantitative Genetics of Anthropometric Traits from the Boas Data" (reprint), 579–594
Murail, P., 495–500
Muslim populations, 427–445
mutation, 657–662

National Health Interview Survey (NHIS), 3–11
Native Americans, 579–594; *see also* Amerindians *and specific populations*
natural selection, 23–42
Neanderthals, 211–235, 287–307
Nei's D_A distance, 389–406
Nei's minimum distance, 389–406
Nei's standard genetic distance, 389–406
Neolithic, 121–140, 339–355, 357–380
Neolithic transition, 639–643
nested models, 799–803
neuromuscular diseases, 23–42
Nievergelt, C. M., 389–406
Nikitin, A. G., 43–58
Noor, S., 427–445
nutrition, 575–578
"Nutrition and the Variation in Level and Age Patterns of Mortality" (reprint), 551–574

O'Connor, K., 551–574, 575–578
Ogriseg, M., 875–898
"One Founder/One Gene Hypothesis in a New Expanding Population: Saguenay (Quebec, Canada)" (reprint), 645–655
origins of agriculture, 211–235
O'Rourke, D. H., 407–426
Ousley, S. D., 579–594, 595–596

paleodemography, 141–157, 211–235, 275–286
paleoecology, 211–235
Paleolithic, 121–140, 287–307, 309–337
Parakanã, 71–88
Pascali, V., 625–638
pastoralism, 597–619, 621–624
Payet, C., 495–500
PCR-RFLP, 43–58
pediatric paradox, 773–776
Peterson, C. P., 829–847
phenotypic correlation, 595–596
"Phylogenetic Analysis of the Evolution of Lactose Digestion in Adults" (reprint), 597–619
phylogenetic comparative methods, 621–624
phylogenetic trees, 621–624
phylogeny, 597–619
phylogeography, 495–500, 639–643
Pichler, I., 875–898
Pinggera, G. K., 875–898
Pleistocene, 825–828
Ploner, F., 875–898
Poisson variation, 13–22
Poles, 43–58
population continuity, 407–426
population density, 357–380, 381–384
population differentiation, 805–824
population dispersal, 181–210
population genetic models, 141–157
population genetics, 23–42, 389–406, 427–445
population growth, 181–210, 211–235, 275–286
population size, 275–286
"Population Size and Rates of Language Change," 259–274
population substructure, 389–406
Portuguese, 71–88
Pramstaller, P. P., 875–898
pregnancy, 463–477
prehistoric Europe, 105–119
prehistory, 309–337
probability theory, 3–11
Procrustes analysis, 389–406

quantitative genetics, 523–546
quantitative risk factors, 869–874
quantitative trait loci (QTLs), 547–550, 849–852, 853–867, 869–874
"Quantitative Trait Nucleotide Analysis Using Bayesian Model Selection" (reprint), 829–847
quantitative trait nucleotides, 853–867
quantitative traits, 523–546

race, 777–798
racial typing, 799–803
radiocarbon dating, 121–140
Rahimy, M. C., 899–909
range expansion, 141–157
Ray, N., 141–157
reaction-dispersal competition model, 181–210
recessive disorders, 657–662
recolonization, 805–824
relative population weights, 735–751
Relethford, J. H., 805–824
Renfrew, C., 381–384

replacement, 407–426
reproductive isolation, 89–95
reproductive skew theory, 339–355
restriction fragment length polymorphisms (RFLPs), 735–751
restriction site polymorphisms (RSPs), 735–751
Réunion Islanders, 495–500
Reynolds distance, 389–406
Rh, 23–42
Rhineland, 357–380
ρ statistic, 911–933
Ribeiro-dos-Santos, A. K. C., 71–88
Ribeiro-Rodrigues, E. M., 71–88
Richerson, P. J., 211–235
Riede, F., 309–337
Rodríguez-Arroyo, G., 447–461
Rodríguez-Larralde, A., 447–461
Romanians, 43–58
Russians, 43–58

Sabater-Lleal, M., 853–867
Saguenay population (Quebec), 657–662
Saguenay region, 645–655
Salzano, F. M., 71–88
San Luis (Argentina), 59–69
Sardinia, 479–493
Scandinavia, 309–337
Schork, N. J., 389–406
seasonality, 463–477
"Seasonality in Birth Weight: Review of Global Patterns and Potential Causes," 463–477
selection, 899–909
senescence, 275–286
sequence data, 829–847
settlement archaeology, 357–380
"The Sex Composition of Two-Children Families: Heterogeneity and Selection for the Third Child—Comment on Stansfield and Carlton (2009)" (letter), 97–100
sex ratio, 3–11, 13–22
Shalev, V., 463–477
Shennan, S., 105–119, 339–355
Shia Muslims, 427–445
short tandem repeats (STRs), 427–445, 799–803
sickle cell disease, 899–909
Sierras Centrales (Argentina), 59–69
single nucleotide polymorphisms (SNPs), 735–751, 799–803, 829–847
site density, 357–380
Smith, S. E., 407–426
social homogamy, 89–95
SOLAR genetics analysis package, 849–852
Soria, J. M., 853–867, 869–874
South America, 59–69. *See also specific countries and populations*
South Amerindian gene geography, 71–88
South Tyrol, 875–898
Souto, J. C., 853–867
spatial and temporal heterogeneity, 121–140
spatial autocorrelation analysis, 639–643
spatial endogamy, 89–95
spatial population ecology, 339–355
SPLATCHE software, 141–157
spread of agriculture, 159–179
Stansfield, W. D., 3–11
"Statistical Genetic Approaches to Human Adaptability" (reprint), 523–546
statistical genomics, 829–847
statistical methods, 523–546
Steele, J., 105–119, 121–140
Stefanov, S. A., 875–898
stopping rule, 3–11
STRs. *See* short tandem repeats
study design, 729–733
Sunni Muslims, 427–445
surfing phenomena, 141–157
surname distribution, 447–461
Suruí, 71–88

Tasmanian effect, 211–235
"Technological Responses of Neanderthals to Macroclimatic Variations (240,000–40,000 BP)," 287–307
Tehrani, J., 159–179
Terwilliger, J. D., 663–728, 729–733
TH01 (*THO1*), 71–88, 427–445
Thionville, M.-D., 495–500
thrombosis, 853–867, 869–874
time delay, 121–140
Tiriyó, 71–88
tool kits, 211–235
Torroni, A., 509–521
Tovo-Rodrigues, L., 71–88
TPOX, 71–88, 427–445
tuberculosis, 899–909
Tuffreau, A., 287–307
two-boy problem, 3–11

Ukraine, 43–58
Ukrainians, 43–58
"Update to Blangero et al.'s 'Quantitative Trait Nucleotide Analysis Using Bayesian Model Selection' (2005): From QTL Localization to Functional Variant Identification," 849–852
"Update to Blangero's 'Statistical Genetic Approaches to Human Adaptability' (1993): A

Unified Theory of Genotype × Environment Interaction, 547–550
"Update to Chikhi et al.'s 'Clinal Variation in the Nuclear DNA of Europeans' (1998): Genetic Data and Storytelling—From Archaeogenetics to Astrologenetics?" 639–643
"Update to Eller et al.'s 'Local Extinction and Recolonization, Species Effective Population Size, and Modern Human Origins' (2004)," 825–828
"Update to Gage and O'Connor's 'Nutrition and the Variation in Level and Age Patterns of Mortality' (1994)," 575–578
"Update to Gage's 'Birth-Weight-Specific Infant and Neonatal Mortality' (2002)," 773–776
"Update to Heyer's 'One Founder/One Gene Hypothesis in a New Expanding Population' (1999)," 657–662
"Update to Holden and Mace's 'Phylogenetic Analysis of the Evolution of Lactose Digestion in Adults' (1997): Revisiting the Coevolution of Human Cultural and Biological Diversity," 621–624
"Update to Konigsberg and Ousley's 'Multivariate Quantitative Genetics of Anthropometric Traits from the Boas Data' (1995)," 595–596
"Update to Long and Kittles's 'Human Genetic Diversity and the Nonexistence of Biological Races' (2003): Fixation on an Index," 799–803
"Update to Soria et al.'s '*F7* Gene and Clotting Factor VII Levels' (2005): Genetic Determinants of Quantitative Traits in Thrombotic Disease," 869–874
"Update to Terwilliger and Göring's 'Gene Mapping in the 20th and 21st Centuries' (2000): Gene Mapping When Rare Variants Are Common and Common Variants Are Rare," 729–733
Urubu-Kaapor, 71–88
U.S. Hispanics, 71–88
U.S. whites, 71–88

Vargiu, R., 479–493
variance components, 853–867
variance-covariance matrices, 595–596
"Variants of the Mannose-Binding Lectin Gene in the Benin Population: Heterozygosity for the p.G57E Allele May Confer a Selective Advantage" (reprint), 899–909
"Variation of the Probability of a Male Birth Within and Between Sibships," 13–22
Videiko, M. Y., 43–58
Vogt, P., 237–258
Volpato, C. B., 875–898
vos Savant, M., 3–11
VWA, 427–445

Waiãpi, 71–88
Wai Wai, 71–88
Wallace, D. C., 509–521
wave of advance model, 159–179
Wendt, K. P., 357–380
Wichmann, S., 259–274
Williams, J. T., 829–847
Willis, C. M., 43–58
World Atlas of Language Structures (WALS), 259–274
Wright's F_{ST} for diploid data, 389–406
Wright's F_{ST} for haploid data, 389–406

Xavante, 71–88

Y chromosome, 875–898
Y-chromosome distribution, 159–179

Zaccaria, I., 899–909
Zimmermann, A., 357–380
Zoé, 71–88
Zoró, 71–88